SEQUENCE LISTING

<110> Gladyshev, V. et al. <120> Mammalian selenoprotein differentially expressed in tumor \cells <130> 56113 <140> <141> <150> 60/080,850 <151> 1998-04-06 <150> PCT/US99/07560 <151> 1999-04-06 <160> 15 <170> PatentIn Ver. 2.0 <210> 1 <211> 162 <212> PRT <213> Homo sapiens <220> <221> SITE <222> (93) <223> Xaa represents selenocysteine <400> 1 Met Ala Ala Gly Pro Ser Gly Cys\Leu Val Pro Ala Phe Gly Lys Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu 40 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp 60 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys\Gly Xaa Lys Leu Gly 90 Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Ash Lys Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val Leu 115 Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu

Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu

160

155

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Arg Ile
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<212 > DNA
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Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu

1 10 15

cgg ttg ttg ttg gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca 97
Arg Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala
20 25 30

gag ttt tca tcg gag gca tgc aga gag tta ggc ttt tct agc aac ttg 145 Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu 35 40 45

ctt tgc agc tct tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg 193 Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu 50 55 60

gat cct gat tgc aga gga tgc tgt cag gag gaa gca caa ttt gaa acc 241
Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Ala Gln Phe Glu Thr
65 70 75

aaa aag ctg tat gca gga gct att ctt gaa gt tgt gga tga aaa ttg 289 Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu 80 85 90 95

gga agg ttc cct caa gtc caa gct ttt gtt agg agt gat aaa ccc aaa 337 Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys 100 105 110

ctg ttc aga gga ctg caa atc aag tat gtc cgt ggt tca gac cct gta 385 Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val 115 120 125

tta aag ctt ttg gac gac aat ggg aac att gct gaa gaa ctg agc att 433 Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile 130 135 140

ctc aaa tgg aac aca gac agt gta gaa gaa ttc ctg agt gaa aag ttg 481 Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu 145 150 155

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Glu Arg Ile
160
aaatqaaata ttacaqcacc tagaaaataa tttagttttg cttgcttcca ttgatcagtc 593
ttttacttga\ggcattaaat atctaattaa atcgtgaaat ggcagtatag tccatgatat 653
ctaaggagtt ggcaagctta acaaaaccca ttttttataa atgtccatcc tcctgcattt 713
gttgatacca ctaacaaaat gctttgtaac agacttgcgg ttaattatgc aaatgatagt 773
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cagatgatta ctatgcctca tgtgctgtgt gctctttgaa aggaatgaca gcagactaca 893
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gcataaaaac tttgtagctt cattattgta aaacatattc aagatcctac agtaagagtg 1073
aaacattcac aaagatttgc gttaa tgaag actacacaga aaacctttct agggatttgt 1133
gtggatcaga tacatacttg gcaaattttt gagttttaca ttcttacaga aaagtccatt 1193
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<213> Homo sapiens
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ttg ttg ttg gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca gag
                                                                   96
Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Glx Ala Glu
ttt tca tcg gag gca tgc aga gag tta ggc ttt tct agc aac ttg ctt
                                                                   144
Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
tgc agc tet tgt gat ett ete gga cag tte aac etg ett cag etg gat
                                                                   192
Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
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gaa cgc ata taa atcttgctta aattttgtcc tatccttttg ttaccttatc

533

cct gat tgc aga gga tgc tgt cag gag gaa gca caa ttt gaa acc aaa

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Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
                      70
aag ctg tat gca gga gct att ctt gaa gtt tgt gga tga aaa ttg gga
                                                                    288
Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa Lys Leu Gly
agg ttc\cct caa gtc caa gct ttt gtt agg agt gat aaa ccc aaa ctg
                                                                    336
Arg Phe Rro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys Leu
                                 105
ttc aga gga\ctg caa atc aag tat gtc cgt ggt tca gac cct gta tta
                                                                    384
Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val Leu
        115
aag oft tig gad gac aat ggg aac att got gaa gaa oig agc att oic
                                                                    432
Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu
    130
                        135
                                             140
aaa tgg aac aca ga& agt gta gaa gaa ttc ctg agt gaa aag ttg gaa
                                                                    480
Lys Trp Asn Thr Asp\Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu
                    150
                                         155
cgc ata taa
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Arg Ile
<210> 4
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<213> Homo sapiens
<220>
<221> SITE
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Asn Leu Leu Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu
Ala Gln Phe Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile\ Leu Glu Val
Cys Gly Xaa Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg
                                                              80
Ser Asp Lys Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg
                                     90
Gly Ser Asp Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala
Glu Glu Leu Ser Ile Leu Lys Trp Asn Thr Asp Ser Val Glu Glu Phe
        115
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                                                 125
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in F
         <210> 7
ij.
         <211> 21
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         <400> 7
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        <223> TGA codon codes for Selenocysteine, Xaa
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Leu Ser Glu Lys Leu Glu Arg Ile

<213> Artificial Sequence

130

<210> 5 <211> 21 <212> DNA

<400> 8

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ggg ctg cgc ttg ctg ctg gcg act gcg ttt caa gcg gtg tct gct ctg

21

21

21

49

1

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Gly Leu Arg Leu Leu Ala Thr Ala Phe Gln Ala Val Ser Ala Leu 20 ggg 🖎 gag ttt gcg tca gag gca tgc aga gag ttg ggt ttc tcc agc Gly Alà Glu Phe Ala Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser aac ttg ctc tgc agc tot tgc gat ott ott gga cag ttt aat otg otc 193 Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu cca ctg gac cct gtt tgc aga ggg tgc tgt cag gaa gaa gca caa ttt 241 Pro Leu Asp Pro Val Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe gaa acc aaa aag ctg tat gca gga gcc atc ctt gaa gtc tgc gga tga 289 Glu Thr Lys Lys Leu\Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly Xaa aaa ttg ggg agg ttc cct caa gtc caa gct ttt gtc aga agt gat aaa 337 Lys Leu Gly Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys 100 ccc aaa ctc ttc aga ggt cta cag atc aag tat gtt cga ggc tca gac 385 Pro Lys Leu Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp 110 115 cct gta cta aag ctt ttg gac gac ac ggg aac att gct gaa gaa cta Pro Val Leu Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu 135 agc atc ctc aaa tgg aac aca gac agt gtg gaa gag ttc ctg agc gag Ser Ile Leu Lys Trp Asn Thr Asp Ser Wal Glu Glu Phe Leu Ser Glu 481 145 150 aag ttg gaa cgcatataaa catgcttagt agttthtata ctaatcaaat 530 Lys Leu Glu 160

gaattatcac agcacctaga caataactta gttttgcatg cttacattgg tcatcctttt 590 tatgtacatc attaatcttc tgacaagaag ctgaagtagc accacagtcc ataatatatc 650 aggatctggc aagcttaagg aacccagctc ttagaaattt ctctttctt acacttgttg 710 ctctcaccag tgaaacgctt tgtaaggagg catctgggta attatgcaaa taagtttgtg 770 ataattgctc cagttctaca aacaacagaa ttttaaatag aggaagtgga taaaaggagac 830 acctcccttg ctgtgtgctc tttgaaagta attgacagaa aactacaaac acgtaggatg 890 ccctgcgcct cagcagcacc caccccagag cctcttggcg tgcccagctt tctttcagt 950 acaagtattt gtagttgta atgaatgtgc cacatacagg ttttgtagct tattattatg 1010 gaacagactg aagatctgca gtacgaatgt aatacttata aaggtttgca ttaatgagga 1070 ttacacagaa aacctttgtt aaggacttgt gtagatctga taattggcaa atttttattt 1130 taaaagtatt cttacagaag agttccattt aagaatgttc acctatagga ccaaaatata 1190

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<210> 9
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<212> PRT
<213> Mus musculus
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<221> SITE
<222> (93)
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Phe Ala Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Pro Leu Asp
Pro Val Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
Lys Leu Tyr Ala Gly Ala Ile Leu Glu\Val Cys Gly Xaa Lys Leu Gly
Arg Phe Pro Gln Val Gln Ala Phe Val Arg Ser Asp Lys Pro Lys Leu
            100
                                105
Phe Arg Gly Leu Gln Ile Lys Tyr Val Arg Gly Ser Asp Pro Val Leu
Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Clu Leu Ser Ile Leu
    130
                        135
Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser\Glu Lys Leu Glu
                                        155
Arg Ile
<210> 10
<211> 20
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<223> Description of Artificial Sequence: PCR primer
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<210> 11

<400> 10

atggcggcag ggcagggtgg

25